

REMARKS/ARGUMENTS

Status of the Claims

Upon entry of the present response, claims 27-35 and 37-38 are pending. Claims 27-35 are withdrawn as directed to a non-elected invention. Claims 37-38 are under examination. No amendments are made to the claims.

Request for Rejoinder

Pursuant to M.P.E.P. § 821.04, Applicants respectfully request rejoinder of method claims 27-35. In accordance with M.P.E.P. § 821.04, Applicants amended claim 27 in a previously submitted response to correspond to the scope of claim 37.

Rejection under 35 U.S.C. § 103(a)

The Examiner has maintained the rejection claims 37 and 38 under 35 U.S.C. § 103(a) as allegedly rendered obvious over U.S. Patent No. 5,858,752 ("Seed") in view of Sasaki, *et al.*, *J Biol Chem* (1994)269:14730-14737 ("Sasaki"). This rejection is respectfully traversed because Seed is not prior art, and Sasaki does not disclose or suggest any murine Fuc-TVII enzyme.

In the Advisory Action mailed on July 24, 2007, the Examiner acknowledged that the Exhibit B accompanying the Rule 131 Declaration of Kevin Gersten submitted on March 20, 2007 shows actual reduction to practice. However, the Examiner has requested additional evidence to show that phage 104 identified in Exhibit B and discussed in the Rule 131 Declaration of Kevin Gersten contains the Fuc-TVII gene. In response, Applicants provide a second Rule 131 Declaration from Dr. John Lowe, co-inventor with and supervisor to Dr. Kevin Gersten and Dr. Shunji Natsuka. Dr. Lowe submits with his Declaration copies from orders of primers used to sequence the Fuc-TVII gene in phage 104.¹ As the Examiner can see, the primers were ordered by co-inventor Dr. Gersten, and the primers are interchangeably referenced

¹ The copies of the orders of the FucT-VII/phage 104 primers, with dates redacted, are attached as Exhibit C. A list of the primers is attached as Exhibit D.

as phage 104 or FucT-VII. The primers include 624B and 625B, discussed in the previous response and Rule 131 Declaration of Kevin Gersten. Dr. Lowe also provides with his Declaration the full sequence of the mouse FucT-VII gene, sequenced from phage 104 and annotated to show the annealing positions of the primers used to sequence the Fuc-TVII gene.² As the Examiner can see, in the annotated FucT-VII gene sequence, the primers as listed in Exhibit D are in bold; forward primers are labeled above the primer sequence and reverse primers are labeled below the primer sequence. Moreover, when the sequence from phage 104 shown in Exhibit E is subject to a BLAST alignment against the mouse genome database, the only transcript that is retrieved is for mouse fucosyltransferase VII (GenBank accession number NM_013524).³ A BLAST alignment also confirms that the sequence of phage 104 shares effectively 100% sequence identity with SEQ ID NO:1 of the present application. Finally, Dr. Lowe provides a notebook page from co-inventor Dr. Shunji Natsuka.⁴ The page from Dr. Natsuka's notebook records a Southern blot of the mouse FucT-VII gene ("mFT7"). This notebook page is another example of the interchangeable reference to the mouse FucT-VII gene and phage 104. That is, it is clear that scientists in Dr. Lowe's laboratory, including co-inventors Drs. Lowe, Gersten and Natsuka, recognized that phage 104 contained the sequence of mouse FucT-VII. The objective sequences of the primers and the full length sequence from phage 104 are consistent with the conclusion that phage 104 contained mouse FucT-VII.

In view of the evidence provided with Dr. Lowe's Declaration and the present response, it is clear that phage 104 referenced in Exhibit B contained the sequence of the mouse FucT-VII gene. The Examiner acknowledges that Exhibit B clearly demonstrates the reduction to practice of the amplification of a sequence encoding the stem and catalytic domains of mouse Fuc-TVII from a mouse nucleic acid sequence captured in phage 104.

Therefore, in accordance with M.P.E.P. § 715.02, Applicants have demonstrated possession of the basic inventive concept of what is claimed before the effective filing date of the Seed reference. In view of the further evidence presented with the present response, Exhibit B

² The annotated sequence of the mouse FucT-VII gene is provided as Exhibit E.

³ BLAST sequence alignments and report for NM_013524 are provided as Exhibit G.

demonstrates using the primers as taught on page 47 of the specification and as claimed to amplify and clone a sequence encoding the stem and catalytic domains of mouse Fuc-TVII. Therefore, the Rule 131 Declarations of Drs. Gersten and Lowe are sufficient to overcome the rejection based on the Seed reference because Seed is not prior art.

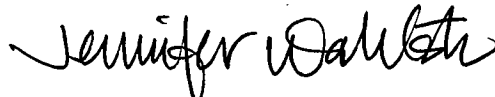
Therefore, for the reasons set forth in the previous responses and herein, Applicants respectfully maintain that the present invention is not obvious over Seed in view of Sasaki because Seed is not prior art. Accordingly, the Examiner is respectfully requested to withdraw this rejection.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance and an action to that end is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



Jennifer L. Wahlsten
Reg. No. 46,226

TOWNSEND and TOWNSEND and CREW LLP
Two Embarcadero Center, Eighth Floor
San Francisco, California 94111-3834
Tel: 415-576-0200
Fax: 415-576-0300
Attachments
JLW:jlw
61182944 v1

⁴ The page from Dr. Natsuka's notebook, with dates redacted, is provided as Exhibit F.

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

Applied Biosystems G 497810

Facility Use Only:

Sequence #

3242 B

Column

Applied Biosystems G 497852

RR

Date Synthesized

D.G.

Today's Date:

Requestor: Gersten

P.I. Name: LOWE

Birthing Dept.: HHMI

Phone Number: 7-4756

Account Number: 921099

Sequence Length: 36

BA

Synthesis Scale: 0.2 umole

Trityl Group: ___ On ___ X ___ Off

Thio-Chemistry: ___ Yes ___ X ___ No

SEQUENCE. 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GCG CCT CGA GCA AAC AGG AAG GAC AGC AGG CTC TGG

User Comments:

ECGF-VII genomic pcr bp 9-34 5' pcr exon 1

Comments to Core Facility:

- 794 Synthesis Setup Listing -

(Version 1.02)

Column 1

Run ID :

Cycle : Cvc01 user

End Proc: End CE

DMT = Off)

Sequence: 3242B

Total bases = 36

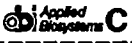
A= 10, G= 13, C= 10, T= 3, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 11142.2

5'> GCG CCT CGA GCA AAC AGG AAG GAC AGC AGG CTC TGG <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 1088 B
Column  425287
Date Synthesized D.C.

Today's Date: Sequence Length: 20
Requestor: Gersten Synthesis Scale: 0.2 umole
P.I. Name: LOWE Trityl Group: ___On ___X___ Off
Billing Dept.: HHMI Thio-Chemistry: ___Yes ___X___ No
Phone Number: 7-4754
Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

TTT GTT TCC GCC CCG GCA TC

User Comments:

104 phage from primer 1042 towards sal site

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 1.01)

Column 3

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 1088B

Total bases = 20

A= 1, G= 4, C= 8, T= 7, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6418.0

✓ 5'→ TTT GTT TCC GCC CCG GCA TC <3'

$A_{260} = .240$

4.2 ul / 958

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

Applied Biosystems C 489928

FACILITY USE ONLY:

Sequence #

9392A

Column

Applied Biosystems C 483082

Date Synthesized

D6

Today's Date:

Requestor: Gersten

P.I. Name: LOWE

Billing Dept.: HHMI

Phone Number: 7-4756

Account Number: 030131

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ___ On ___ X ___ Off

Thio-Chemistry: ___ Yes ___ X ___ No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GCT AGA TAG TTT CTG ATG GC

OD₂₆₀ 1.00 = 1.41

User Comments:

Fuct7-1

25/1ml

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 2.00)

Column 2

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 9392A

Total bases = 20

A= 4, G= 6, C= 3, T= 7, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6158.0

5'> GCT AGA TAG TTT CTG ATG GC <3'

Synthesis Request Sheet

⑬

Thio-Chemistry: ☐ Yes ☒ X ☐ No

46/954

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 8660A
Column Applied Biosystems C 489821
Date Synthesized DM Ⓢ

Today's Date: Sequence Length: 20
Requestor: Gersten Synthesis Scale: 0.2 umole
P.I. Name: LOWE Trityl Group: ___On ___X___ Off
Billing Dept.: HHMI Thio-Chemistry: ___Yes ___X___ No
Phone Number: 7-4756
Account Number: 030131

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CAG GGC ACT TCT GAG GTG CC

User Comments:
Fuc-TVII bp424 sequencing primer towards 3' end

Comments to Core Facility:

$\frac{1}{100} = .01$

25/1ml

- 394 Synthesis Setup Listing - (Version 1.01)

Column 3

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 8660A

Total bases = 20
A= 3, G= 7, C= 6, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6573.0

5'> CAG GGC ACT TCT GAG GTG CC <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

Applied Biosystems G 495751

FACILITY USE ONLY:

Sequence #

9393A

Column

Applied Biosystems G 472563

Date Synthesized

D.G.

Today's Date:

Requestor: Gersten

P.I. Name: LOWE

Billing Dept.: HHMI

Phone Number: 7-4756

Account Number: 030131

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ___ On ___ X ___ Off

Thio-Chemistry: ___ Yes ___ X ___ No

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

AAC AGC AGC CTT GTC ACG TG

User Comments:

Fuct7-2

OD $260 / 1100 = .156$

26/1000

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 2.00)

Column 3

Run ID :

Cycle : Cyc01 user

End Proc: End CE

Sequence: 9393A

(DMT = Off)

Total bases = 20

A= 5, G= 5, C= 6, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6078.0

5'> AAC AGC AGC CTT GTC ACG TG <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

986 B

Column

 C 421275

Date Synthesized

(8)

Today's Date:

Sequence Length: 20

Requestor: Gersten

Synthesis Scale: 0.2 umole

P.I. Name: LOWE

Trityl Group: ___On ___X___ Off

Billing Dept.: HHMI

Thio-Chemistry: ___Yes ___X___ No

Phone Number: 7-4778

Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CAG CCA TAG TCT CAC GTG AC

User Comments:

104 sal-eco from 887 primer towards sal site (5' UT)

Comments to Core Facility 394 Synthesis Setup Listing -

(Version 1.01)

Column 3

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 986B

Total bases = 20

A= 5, G= 4, C= 7, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6536.0


5'→ CAG CCA TAG TCT CAC GTG AC <3'

.272

37ul / 963

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 672 B
Column  410014
Date Synthesized *D.K.*

Today's Date: Sequence Length: 20
Requestor: Gersten Synthesis Scale: 0.2 umole
P.I. Name: LOWE Trityl Group: ☐ On ☒ Off
Billing Dept.: HHMI Thio-Chemistry: ☐ Yes ☒ No
Phone Number: 7-4778
Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CGA AGT GTA GGA AGT GAT CC

User Comments:

104 from 15/52 large (Xho-Kpn) towards 3' end

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 2

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 672B

Total bases = 20

A= 6, G= 7, C= 3, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6693.0

✓ 5'→ CGA AGT GTA GGA AGT GAT CC <3'

$L_{260} = .304$

33 *al* 1967

Synthesis Request Sheet

35 ul / 965

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8993

Product Information

Length: 20

Oligonucleotide Sequence:
AGG AAG CTT ABC TAA AAG CT

Comments:

104 phage from t7 primer towards 3' end of gene (5' ut towards gene)

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8993
Thank you for using the HHMI Biopolymer Facility.

Use 10459c PTZR DNA

$A_{260} = .264$

38 μ l / 962

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 734-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

671 B

Column

Applied Biosystems C 410554

Date Synthesized

D.G.

Today's Date:

Sequence Length: 20

Requestor: Gersten

Synthesis Scale: 0.2 umole

P.I. Name: LOWE

Trityl Group: ☐ On ☒ Off

Billing Dept.: HHMI

Thio-Chemistry: ☐ Yes ☒ No

Phone Number: 7-4778

Account Number: 921099

SEQUENCE, 5' → 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GCA AAG CTA TAG CTT GTA GC

User Comments:

104 from 15/52 (EcoRI) towards 5' end

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 1

Run ID :

Cycle : Cvc01 user

End Proc: End CE (DMT = Off)

Sequence: 671B

Total bases = 20

A= 6, G= 5, C= 4, T= 5, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6629.0

✓ 5' → GCA AAG CTA TAG CTT GTA GC <3'

$A_{260} = .319$

38 ul / 969

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 3511 B
Column ~~Applied Biosystems~~ G 404333
Date Synthesized SAS (BA)
Date Submitted: Sequence Length: 20
Requestor: Kelly Synthesis Scale: 0.2 umole
Phone Number: 74756
Account Number: 921099 Trityl Group: No
P.I. Name: LOWE HPLC Purify: No
Billing Dept.: HHMI Thio-Chemistry: No
Center Membership: None
Center/Project Related Research: No

SEQUENCE, 5' -> 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

AGC CTG GAC CTG AGG CTG GG

User Comments:
FT7-1

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 2.00)

Column 2

Run ID :
Cycle : Cvc01 user
End Proc: End CE (DMT = Off)
Sequence: 3511B

Total bases = 20

A= 3, G= 9, C= 5, T= 3, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6191.0

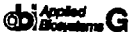
5'> AGC CTG GAC CTG AGG CTG GG <3'

OD₂₆₀ 1/100 .102

40/1ml

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 946 B
Column  439483
Date Synthesized D.G.

Today's Date: Sequence Length: 20
Requestor: Gersten Synthesis Scale: 0.2 umole
P.I. Name: LOWE Trityl Group: ___On ___X___ Off
Billing Dept.: HHMI Thio-Chemistry: ___Yes ___X___ No
Phone Number: 7-4778
Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

TCC TTC CCT TTC CAG ACT GG

User Comments:
104 sac sequencing from 910 towards cat exon

Comments to Core Facility:

- 394 Synthesis Setup Listing - (Version 1.01)

Column 4

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 946B

Total bases = 20
A= 2, G= 3, C= 8, T= 7, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)



MW: 6419.0

✓5' TCC TTC CCT TTC CAG ACT GG <3'

$A_{260} = .204$

49/957

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 715 B
Column  406550
Date Synthesized D.B. 

Today's Date: Sequence Length: 20
Requestor: Gersten Synthesis Scale: 0.2 umole
P.I. Name: LOWE Trityl Group: ___On ___X___ Off
Billing Dept.: HHMI Thio-Chemistry: ___Yes ___X___ No
Phone Number: 7-4778
Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GGG AAG GAG TCT GTG TGT CC

User Comments:
104 pcr of t cell large frag from sp6 seq

Comments to Core Facility:

COLUMN Z SET-UP
VERSION 2.01

USER_NAME:
CYCLES USED: SSCEAF36- 1
ENDING METHOD: Trityl OFF, Auto
ENDING PROCEDURE: DEPCRE03
SEQUENCE NAME: 715B
SEQUENCE LENGTH: 20
DATE:
TIME:
COMMENT:

✓ 5'- GGG AAG GAG TCT GTG TGT CC -3'

$A_{260} = .304$

33ul / 967

Synthesis Request Sheet

5' > ACC TTG GGC TGA ACC TAC AG <3'

Synthesis Request Sheet

2932 B

Applied Biosystems C 460602

Chew Berry

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: ☐ On ☒ Off

Thio-Chemistry: ☐ Yes ☒ No

[illegible]

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

sequence primer proximal to exon 1 S.D towards 5' UT (FT-VII)

Comments to Core Facility:

(Version 1.01)

Sequence: 2932B

A= 4, G= 5, C= 5, T= 6, S= 0, b= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6563.0

5' > CCT TGA ACT GTA GGT TCA GC <3'

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 8661A
Column C 484064
Date Synthesized CH (N)
Today's Date: Requestor: Gersten Sequence Length: 20
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HHMI Trityl Group: On X Off
Phone Number: 7-4756 Thio-Chemistry: Yes X No
Account Number: 030131

SEQUENCE, 5' -> 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

TTT TCT AGA GGT GGC AGA AC

User Comments: $1/100 = .443$
fuc-tvii sequencing primer towards 3' end (bp 1333)

Comments to Core Facility: 22.57 / 1 ml

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 3

Run ID :
Cycle : Cyc01 user
End Proc: End CE (DMT = Off)
Sequence: 8661A

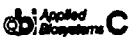
Total bases = 20

A= 5, G= 6, C= 3, T= 6, 5= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 6642.0

5'> TTT TCT AGA GGT GGC AGA AC <3'

Synthesis Request Sheet

FACILITY USE ONLY:	Sequence #	911 B
	Column	 426226 -----
	Date Synthesized	DC-----

Today's Date:	Sequence Length:	20
Requestor: Gersten	Synthesis Scale:	0.2 umole
P.I. Name: LOWE	Trityl Group:	___On ___X___ Off
Billing Dept.: HHMI	Thio-Chemistry:	___Yes ___X___ No
Phone Number: 7-4778		
Account Number: 921099		

SEQUENCE, 5' -> 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GGA CCT GTG CTC CCA GAT CC

User Comments:


104 sequencing from sac 9076 primer towards 5' exon

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 2

Run ID :
 Cycle : Cyc01 user
 End Proc: End CE (DMT = )
 Sequence: 911B

Total bases = 20

A= 3, G= 5, C= 8, T= 4, 5= 0, 6= 0, 7= 0, 8= 0
 (mixed bases= 0)

MW: 6495.0

✓ 5' > GGA CCT GTG CTC CCA GAT CC < 3'

Aug 2, 215

47 ml / 953

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 9077

Product Information

Length: 20

Oligonucleotide Sequence:
AAG GGA TCA CTT CTG CTC AG

Comments:
104phage from 8952 towards 5' end of gene

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 4

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 9077
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.219$

46 ul / 954

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 9076

Product Information

Length: 20

Oligonucleotide Sequence:
TGC TT(CAST) CCT TCA GGA AAA GG

Comments:
104phage from 8952 towards 5' ut

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:
Date Synthesised:
Number of Day(s) in the System: 4

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 9076
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .217$

461954

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

3445 B

Column

Applied Biosystems G 404852

Date Synthesized

SAS

BB

Date Submitted:

Requestor: Kelly

Phone Number: 74756

Account Number: 921099

P.I. Name: LOWE

Billing Dept.: HHMI

Sequence Length: 20

Synthesis Scale: 0.2 umole

Trityl Group: No

HPLC Purify: No

Thio-Chemistry: No

Center Membership: None

Center/Project Related Research: No

SEQUENCE, 5' → 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

CTA GCT GGT CAT TTC TAG GG

User Comments:
ft7-1

Comments to Core Facility:

DNA SEQUENCE 1

NUMBER OF BASES: 20

BASES USED: A=3 C=4 G=6 T=7 X=0

DALTONS: 5115

TIME:

DATE:

5' → CTA GCT GGT CAT TTC TAG GG < 3'

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8953

Product Information

Length: 20

Oligonucleotide Sequence:
TCA ATT CCC TCT TTG AGC AG

Comments:

104 phage from 8903 primer towards 3' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8953
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 1.290$

38ul / 965ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8952

Product Information

Length: 20

Oligonucleotide Sequence:
ATC AAC CAC TAT CCA ATC CT

Comments:

104 phage from primer B903 towards 5' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8952
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .290$

75ul / 965ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8904

Product Information

Length: 20

Oligonucleotide Sequence:
TGA CAA TTC CAG AAG GCT CC

Comments:

104 phage from primer 8874 towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8904
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .272$

37 ml / 963

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8903

Product Information

Length: 20

Oligonucleotide Sequence:
GGC CAG GCA CTC ACC AAT AC

Comments:

104 phage from primer 8874 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8903
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .292$

35 μ l / 965

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8902

Product Information

Length: 20

Oligonucleotide Sequence:
TTA TTC TGC TTC AGG GTA CC

Comments:

104 phage from primer 8874 towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8902
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .297$

342 / 966

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8875

Product Information

Length: 20

Oligonucleotide Sequence:
ATC TGC ACT GGC CTT TCA CC

Comments:

104 phage from primer 8850 towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8875
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.300$

33 μ l / 967 μ l

11 G/c

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

9 G/K
H AT

42

Synthesis Request Sheet

FACILITY USE ONLY:

Sequence #

524 B

Column

Applied Biosystems C 416455

Date Synthesized

D.G.

Today's Date:

Sequence Length: 41

Requestor: Gersten

Synthesis Scale: 0.2 umole

P.I. Name: LOWE

Tritvl Group: ___On ___X___ Off

Billing Dept.: HHMI

Thio-Chemistry: ___Yes ___X___ No

Phone Number: 7-4778

Account Number: 921099

SEQUENCE, 5' → 3', IN TRIPLETS (* PLEASE START WITH A TRIPLET *)

GGG CCG ATC CCA CCA TCC TTA TCT GGC ACT GGC CTT TCA CC

User Comments:

phage 104 PCR primer (FOR AB) from nt 292

Comments to Core Facility:

- 394 Synthesis Setup Listing -

(Version 1.01)

Column 4

Run ID :

Cycle : Cyc01 user

End Proc: End CE (DMT = Off)

Sequence: 624B

Total bases = 41

A= 6, G= 8, C= 17, T= 10, S= 0, 6= 0, 7= 0, 8= 0
(mixed bases= 0)

MW: 13246.2

Run 411

✓ 5' → GGG CCG ATC CCA CCA TCC TTA TCT GGC ACT GGC CTT TCA
CC 3'

A₂₆₀ = .505

200 25ul 175ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8874

Product Information

Length: 20

Oligonucleotide Sequence:
TGG TGA GTG TGG ACT GAG GC

Comments:

104 phage from primer 8850 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8874
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .300$

33 ul / 967

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8867

Product Information

Length: 20

Oligonucleotide Sequence:
GCT AGC AGG CTC CGG TTA GC

Comments:
104phage from 8770primer (b sequence) towards 5' end of gene

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8867
Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .259$$

38ul / 962

Report for Synthetic Oligonucleotide

Date:

Investigator: LDWE
Individual User: Gersten

System Id: 8851

Product Information

Length: 20

Oligonucleotide Sequence:
CCT TGG GTC TGG GCC TCC AT

Comments:

104 phage from B770 primer towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8851
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .281$

36 μ l /

176K

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8850

Product Information

Length: 20

Oligonucleotide Sequence:
AAG CGA TAG AGA CCA TGG GT

Comments:

104 phage from 8770 primer towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8850
Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .264$$

39 ul / 962

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8771

Product Information

Length: 20

Oligonucleotide Sequence:
GGC CCA CAT CCC CAC TAC CG

Comments:

104 phage from B715 sequence towards 3' end (towards rp2 primer sequence)

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8771
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.255$

39 μ l
961

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8852

Product Information

Length: 20

Oligonucleotide Sequence:
CAC GCT GCT GCC GCT CCT GG

Comments:

104 phage from B715 primer towards 5' end of gene (replace primer B77)

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8852
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .265$

38 ul / 962

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8714

Product Information

Length: 20

Oligonucleotide Sequence:
GCA TCG GGA CTA CAT CAC TG

Comments:

104pst from rp2 sequence towards the 3' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8714
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .266$

38ul oligo
962ul H_2O

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8715

Product Information

Length: 20

Oligonucleotide Sequence:
AGC CCC AGG CAT TGC GCC AG

Comments:

104pst from rp2 primer towards the 5' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8715
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .297$

33 μ l dig
967 μ l H₂O

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8848

Product Information

Length: 20

Oligonucleotide Sequence:
AAC TGG CTG TCT TCC TCG TC

Comments:

104phage from primer 8714 towards 3' end

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8848
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .299$

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8849

Product Information

Length: 20

Oligonucleotide Sequence:
CAC GAT AAC GAC TCT CAT TC

Comments:
104 phage from primer B714 towards 5' end

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 1

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8849
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .283$

35ul / 965

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8868

Product Information

Length: 20

Oligonucleotide Sequence:
CTG GAG GGA AGC GCT TCT GC

Comments:

104 phage from 8714 (a sequence) towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8868
Thank you for using the HHMI Biopolymer Facility.

$T_m = 60$

$A_{260} = 0.330$

30.2/970

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8876

Product Information

Length: 20

Oligonucleotide Sequence:
CAA GTA AGG GTA GCG GGC AC

Comments:

104 phage from primer 8848 towards 5' end of gene

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

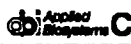
If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8876
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.287$

35ul / 965ul

BIOMEDICAL RESEARCH CORE FACILITIES
DNA SYNTHESIS CORE 2562 MSRB II 764-1461

Synthesis Request Sheet

FACILITY USE ONLY: Sequence # 625 B
Column  C 407370
Date Synthesized D.G.

Today's Date: Requestor: Gersten Sequence Length: 43
P.I. Name: LOWE Synthesis Scale: 0.2 umole
Billing Dept.: HHMI Trityl Group: ___ On ☒ Off
Phone Number: 7-4778 Thio-Chemistry: ___ Yes ☒ No
Account Number: 921099

SEQUENCE, 5'→ 3', IN TRIPLETS (* PLEASE START WITH A TRIFLET *)

GCG CGG ATC CTC ATC AAG CCT GGA ACC AGC TTT CAA GGT CTT C

User Comments:
104 phage PCR (for ab) from stop codon

Comments to Core Facility:

COLUMN 1 SET-UP
VERSION 2.01

USER_NAME:
CYCLES USED: SSCEAF3I- 1
ENDING METHOD: Trityl OFF, Auto
ENDING PROCEDURE: DEPCRE03
SEQUENCE NAME: 625B
SEQUENCE LENGTH: 43
DATE:
TIME:
COMMENT:

✓ 5' GCG CGG ATC CTC ATC AAG CCT GGA ACC AGC TTT CAA

GGT CTT C -3'

A₂₆₀ = 0.662

19 ul / 81 ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8905

Product Information

Length: 20

Oligonucleotide Sequence:
CAG GAA TTC AGG ATA TAA GG

Comments:

104 phage from primer 8868 towards 3' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8905
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = 0.312$

32 μ l / 968

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8877

Product Information

Length: 20

Oligonucleotide Sequence:
GGT AGT GCC ATG GTG ACC AA

Comments:

104 phage from primer 8848 towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 2

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8877
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .318$

31ul / 969ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8954

Product Information

Length: 20

Oligonucleotide Sequence:
AGG TTG CAG ATG CAC CCT CT

Comments:

104 phage from primer 8905 towards 3' ut

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 4

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8954
Thank you for using the HHMI Biopolymer Facility.

$$A_{260} = .272$$

37ul / 963ul

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8967

Product Information

Length: 20

Oligonucleotide Sequence:
GTA CTA GAG GGT GCA TCT GC

44+

Comments:

104 phage from rp2 primer (sac insert) towards 5' end of gene

Trityl Group: Off

Synthesis Scale: 0.2 Micromole Scale

Date Received:

Date Synthesised:

Number of Day(s) in the System: 5

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8967
Thank you for using the HHMI Biopolymer Facility.

$T_a = 56$

use 104 sac 11219

$A_{260} = .230$

440/956

Report for Synthetic Oligonucleotide

Date:

Investigator: LOWE
Individual User: Gersten

System Id: 8713

Product Information

Length: 20

Oligonucleotide Sequence:
ACC ACT CAA GCA AGG CTC TC

Comments:
104pstt7 towards rp2 primer

Trityl Group: Off Synthesis Scale: 0.2 Micromole Scale

Date Received:
Date Synthesised:
Number of Day(s) in the System: 3

If you have any problems, contact the Biopolymers Facility
Your assigned System Id number is 8713
Thank you for using the HHMI Biopolymer Facility.

$A_{260} = .327$

31 ul digo
969 ul H₂O

Primers used to sequence the mouse FucTVII genomic sequence in their order of appearance in the sequence.

3242
1088B
9392A
1042
8660A
9393A
986B
672B
887B
8993
671B
3511B
945B
715B
2931
2932
8661A
911B
9077
9076
3445B
8953
8952
8904
8903
8902
8875
624B
8874
8867
8851
8850
8771
8852
8714
8715
8848
8849
8868
8876
625B
8905
8877
8954
8967
8713

EXHIBIT E: Mouse FucT-VII gene, from phage 104, annotated with DNA sequencing primers used to sequence the phage, with start and stop codons, and with relevant restriction sites. Mouse genomic DNA sequence displayed from position 25,277,900 to 25,282,400 containing the coding sequence for the mouse FucT-VII gene

```

CTACCCTGCT CTGGTTGGAC GAGGGTCCAC AAGGTCTCTT AGGCTGGGTA GAATAGAATG 60
GATGGGACGA GACCAACCTG CTCCCAGGTG TTCCAGAGAA TCCGACCCAT CTTATCTTAC

TGTGATCCTG ATCCTGGAAC CCCAGATGTA AAGCTGGGTT TGGGTGCCCT TGTGAGTGAG 120
ACACTAGGAC TAGGACCTTG GGTCTACAT TTCGACCCAA ACCCACGGGA ACACTCACTC

GAGGCCTGGT GAGGTGAGGT GGTATGTTGA GGTCCCCTGG CTTTCCCTTT GACTCATGAT 180
CTCCGGACCA CTCCACTCCA CCATACAAC CTAGGGGACC GAAAGGGAAA CTGAGTACTA

GTCTCACATT CCCCCACCC CCTTTTCCAT CCTGACCCCA TTTCTGAGCT AAATTTCCGA 240
CAGAGTGTA GGGGGGTGGG GGAAAAGGTA GGACTGGGGT AAAGACTCGA TTTAAAGGCT

ACTGACTCCT CAGTTGGCAA GTTCTCATGG TCAGGTGCCC TACAGTTAAC AGACCTGTG 300
TGA CTGAGGA GTCAACCGTT CAAGAGTACC AGTCCACGGG ATGTCAATTG TCTGGGACAC

GGACCCTCCT CCAAAC TGAG CTGGCATGGG GAGGGGGTCA GTATAACAGC AAGGCAGATG 360
CCTGGGAGGA GGT TTGACTC GACCGTACCC CTCCCCCAGT CATATTGTCG TTCCGTCTAC

TGGGGGAGGT TCCTTCAAAT CCACCCAGGA AGGGAAGAGC ATGTGGGCGT GGGTGAGGCT 420
ACCCCTCCA AGGAAGTTTA GGTGGGTCTT TCCCTTCTCG TACACCCGCA CCCACTCCGA
3242B
GGGGCAAAGG CCCCAGCCAG CCTGGCGGCA CAAACAGGAA GGACAGCAGG CTCTGGCAGC 480
CCCCGTTTCC GGGGTGCGTC GGACCGCCGT GTTTGTCTTT CCTGTCTGTC GAGACCGTCG
PstI
CAGAAGCCTG TGGCCCCAAG CTGGCAGGAT GGCCCCCTTC CTGCAGGTCC CCCACAGCCT 540
GTCTTTCGGAC ACCGGGGTTC GACCGTCCTA CCGGGGGAAG GACGTCCAGG GGGTGTCGGA

TCTGGGTTCC TGACACGAGA GAAGAGGTGG GCGGGGGTGA AGTGAACCTT GAAGCCAAAA 600
AGACCCAAGG ACTGTGCTCT CTTCTCCACC CCGCCCCACT TCACTTGAGA CTTCGGTTTT

TGTGACTCTC CTGGGGTCAC CAGCTTGGGG AGAGGTGAAG AAAGATGCCG GGGCGGAAAC 660
ACACTGAGAG GACCCAGTG GTCGAACCCC TCTCCACTTC TTTCTACGGC CCCCGCTTTG
EcoRI 1088B
AAAGGGGCAG ATATCACTAT GGTATCTTA CTAAGCACAG AGTAACTGAA AAAGCAAGGG 720
TTTCCCCGTC TATAGTGATA CCAATAGAAT GATTCGTGTC TCATTGACTT TTTCGTTCCC
9392A
TACCGCTGCC CACCTCGTGC CCACCTTACG TTATACCTCA AACCAGCTAG ATAGTTTCTG 780
ATGGCGACGG GTGGAGCACG GGTGGAATGC AATATGGAGT TTGGTCGATC TATCAAAGAC

ATGGCACCCA TACCCTCCCT TCCCCTTTAG GCATTGCGCA AGCTCTCCAC CACAATCTGG 840
TACCGTGGGT ATGGGAGGGA AGGGGAAATC CGTAACGCGT TCGAGAGGTG GTGTTAGACC
1042B 8660B
AAGTTATACC CTGCGAGGGG ATGGGCAGGG CACTTCTGAG GTGCCAATCA GCCTGCACTC 900
TTCAATATGG GACGCTCCCC TACCCGTCCC GTGAAGACTC CACGGTTACT CGGACGTGAT
9393A
GCCTCTGCCC TGGCCATGGC ACTGCTGTCA GTTTCTTGGT ACCTGTCTCA ACAGCAGCCT 960
CGGAGACGGG ACCGGTACCG TGACGACAGT CAAAGAACCA TGGACAGAGT TGTCGTCGGA

TGTCACGTGA GACTATGGCT GCGGTGGGG GTGGGGGCAG GAATCCTAGA AGCACAGGAG 1020
ACAGTGCACT CTGATACCGA CCGCCACCCC CACCCCGTC CTTAGGATCT TCGTGTCTC

```

EXHIBIT E

	986B	672B				
TGACATAGGG	TCGGGTCGGG	CAGAGCGAAG	TGTAGGAAGT	GATCCCCAAA	GGGATGCTGG	1080
ACTGTATCCC	AGCCCAGCCC	GTCTCGCTTC	ACATCCTTCA	CTAGGGGTTT	CCCTACGACC	
				SacI		
GGACGATCTG	GCCAACACTG	TCCTCCCAT	CAAAACTCCC	AGTCTGGAGC	TCTGGGACAT	1140
CCTGCTAGAC	CGGTTGTGAC	AGGAGGGTAA	GTTTTGAGGG	TCAGACCTCG	AGACCCCTGTA	
GGACAAGCCA	GGCCTGCTAT	TCTCCATACA	GGGCTCCATA	GTGTCTGGCT	CAGCAGAGTG	1200
CCTGTTTCGGT	CCGACGATA	AGAGGTATGT	CCCGAGGTAT	CACAGACCGA	GTCGTCTCAC	
	8993				887B	
GGGGATCTGG	TGGGGATGGA	GGAAGCTTAG	CTAAAAAGCTT	TGTATAGGCT	GAAGCTCTGA	1260
CCCCTAGACC	ACCCCTACCT	CCTTCGAATC	GATTTTCGAA	ACATATCCGA	CTTCGAGACT	
GTGACCCCTGC	TGGGCCACCC	TACCCCTGGTC	TGGGCTGGGT	CATTGCATCC	CCAGATTGGA	1320
CACTGGGACG	ACCCGGTGGG	ATGGGACCAG	ACCCGACCCA	GTAACGTAGG	GGTCTAACCT	
AGGCTTGGTG	AGATGGAGAG	GAACCTTGGC	TACAAGCTAT	AGCTTTGCCC	ACCAGAGCCT	1380
TCCGAACCAC	TCTACCTCTC	CTTGGAACCG	ATGTTTCGATA	TCGAAACGGG	TGGTCTCGGA	
	3511B			671B		
GCTGGAGGGG	AATCAAACAA	GCCTGGACCT	GAGGCTGGGA	CTAGCTTTCC	TGTTTCTGGA	1440
CGACCTCCCC	TTAGTTTGT	CGACCTGGA	CTCCGACCT	GATCGAAAGG	ACAAAGACCT	
Start codon						946B
GTGGATGCCA	ACCCCTTGCC	CACCAGCCTG	CCTGTCCACG	CCAGGGACAC	ACAGACTCCT	1500
CACCTACGGT	TGGGGGACGG	GTGGTCCGAC	GGACAGGTGC	GGTCCCTGTG	TGTCTGAGGA	
TCCCTTTCCA	GACTGGAAAG	CCCCCTCCTG	GGAGAGCAGG	AAGGAAGCAA	CCTGCAACTC	1560
AGGGAAAGGT	CTGACCTTTC	GGGGGAGGAC	CCTCTCGTCC	TTCTTTCGTT	GGACGTTGAG	
715B	2931B					
TTCCAGCCCT	GGACCTTGGG	CTGAACCTAC	AGTTCAAGGT	TTGTATGCTC	ACAGGTCTTG	1620
AAGGTCGGGA	CCTGGAACCC	GACTTGGATG	TCAAGTTCCA	AACATACGAG	TGTCCAGAAC	
			2932B		PstI	
GCAGGGAAAAG	ATAAGAATCC	CCAGGGCACC	CTCCCCCCCCG	CCCCCCAGTC	CACTGCAGGT	1680
CGTCCCTTTC	TATTCTTAGG	GGTCCCGTGG	GAGGGGGGGC	GGGGGGTCAG	GTGACGTCCA	
AGCTCCTGGG	TCTGCCCTTC	AGGGCAAGTG	CTGACGCTCC	ATCAGACTGT	GATGGGGCCC	1740
TCGAGGACCC	AGACGGGAAG	TCCCGTTCAC	GACTGCGAGG	TAGTCTGACA	CTACCCCGGG	
			8661A			
TTTTCTGAGG	ATGACAATTC	TGAGAACAAG	GCATTTTTCT	AGAGGTGGCA	GAACAGCATT	1800
AAAAGACTCC	TACTGTTAAG	ACTCTTGTTT	CGTAAAAAGA	TCTCCACCGT	CTTGTCGTAA	
TTGTGATGCC	CGAGGATCTG	GGAGCACAGG	TCCAGCTTAA	TGAGGGATTG	GAGGAAGTGG	1860
AACACTACGG	GCTCCTAGAC	CCTCGTGTCC	AGGTCGAATT	ACTCCCTAAC	CTCCTTCACC	
			911B			
GTATCATCAT	TACAGGGAGG	GGCCTCTGTG	GCCTCCTGGG	AAAATGCAGT	TGCTCTCTTT	1920
CATAGTAGTA	ATGTCCCTCC	CCGAGACAC	CGGAGGACCC	TTTTACGTCA	ACGAGAGAAA	
				9077		
GGGTGGCCTG	GGGTTGTGTG	GTGGGCAGAG	GACGGAGGTG	CTCATTGGGG	GAAGGGATCA	1980
CCCACCGGAC	CCCAACACAC	CACCCGTCTC	CTGCCTCCAC	GAGTAACCCC	CTTCCCTAGT	
CTTCTGCTCA	GAGTGCTCGC	AAGGGCCTTT	CCTTTTCTCTG	AAGGCAAGCA	GGCCTCCTCC	2040
GAAGACGAGT	CTCACGAGCG	TTCCCGGAAA	GGAAAAGGAC	TTCCGTTTCGT	CCGGAGGAGG	
			9076	3445B		
TCCTCCTCTT	CCTCCTTCTC	CTCTTCTCTC	TCTTTCTCCA	TATGCCTAGC	TGGTCATTTC	2100
AGGAGGAGAA	GGAGGAAGAG	GAGAAGGAGG	AGAAAGAGGT	ATACGGATCG	ACCAGTAAAG	

EXHIBIT E

					8953	
TAGGG ACCAG	CATGGTTGGG	AAGGGGGCCT	TGTCTTGGCC	TTCCTCTTGT	CTCAATTCCC	2160
ATCCCTGGTC	GTACCAACCC	TTCCCCCGGA	ACAGAACCGG	AAGGAGAACA	GAGTTAAGGG	
TCTTTGAGCA	GAAGAC GGGG	TGGGTGGGGT	AGGGTTGGAT	AGTGGTTGAT	GCCAAAGATT	2220
AGAAACTCGT	CTTCTGCCCC	ACCCACCCCA	TCCCAACCTA	TCACCAACTA	CGGTTTCTAA	
			3512B	8952		
GAAGGGGTAG	GGCGGGGCAG	AAGTGGGAAG	GTCCCTGGCT	TCCTCACCTT	GGTAGATGGT	2280
CTTCCCCATC	CCGCCCCGTC	TTCACCC TTC	CAGGGACCGA	AGGAGTGGAA	CCATCTACCA	
GAGGAGCCCC	AGAGGTTGAG	CTGAGCAGCA	GCTGTGATTT	CAGGGTGCCT	CTGTTGGAGA	2340
CTCCTCGGGG	TCTCCAACTC	GACTCGTCGT	CGACACTAAA	GTCCCACGGA	GACAACCTCT	
			8904			
GGTGCTGTG	ATTTGAAAAT	CTTCTTTCCT	TGGTGACAAT	TCCAGAAGGC	TCCAGATGAA	2400
CCGACGACAC	TAAACTTTTA	GAAGAAAGGA	ACCACTGTTA	AGGTCTTCCG	AGGTCTACTT	
		AflII				
TTGTATTGGT	GAGTGCCTGG	CCCTTAAGCA	GTCCCAGCTG	GGGATGATGG	GGATTTATGG	2460
AACATAACCA	CTCACGGACC	GGGAATTTCG	CAGGGTCGAC	CCCTACTACC	CCTAAATACC	
		8903	8902	KpnI		
GTGTCCCTGA	GCCTAGGGTG	ACAGGGCCTC	TCCTTTTTTT	TTTATTCTGC	TTCAGGGTAC	2520
CACAGGGACT	CGGATCCAC	TGTCCCGGAG	AGGAAAAAAA	AAATAAGACG	AACTCCCATG	
CACCCACCA	GGAGGCTGCG	GGCCTGGGGC	GGCCTAGCTG	GAGGAGCAAC	ATTCATGGTA	2580
GTGGGGTGGT	CCTCCGACGC	CCGGACCCCG	CCGGATCGAC	CTCCTCGTTG	TAAGTACCAT	
ATTTGGTTTT	TCTGGCTGTG	GGGATCAGCT	CCTGGAAGTG	CCCCTGTGCC	TCAGTCCACA	2640
TAAACCAAAA	AGACCGACAC	CCCTAGTCGA	GGACCTTCAC	GGGGACACGG	AGTCAGGTGT	
624B	8875					
CTCACCATCC	TTATCTGGCA	CTGGCCTTTC	ACCAACCGGC	CGCCAGAGCT	ACCTGGTGAC	2700
GAGTGGTAGG	AATAGACCGT	GACCGGAAAG	TGTTTGGCCG	GCGGTCTCGA	TGGACCACTG	
	8874					
ACCTGCACTC	GCTATGGCAT	GGCCAGCTGC	CGTCTGAGTG	CTAACCGGAG	CCTGCTAGCC	2760
TGGACGTGAG	CGATACCGTA	CCGGTCGACG	GCAGACTCAC	GATTGGCCTC	GGACGATCGG	
					8867	
AGTGCTGATG	CTGTGGTCTT	CCACCACCGT	GAGCTGCAAA	CCCGGCAATC	TCTCCTACCC	2820
TCACGACTAC	GACACCAGAA	GGTGGTGGCA	CTCGACGTTT	GGGCCGTTAG	AGAGGATGGG	
		8851				
CTGGACCAGA	GGCCACACGG	ACAGCCTTGG	GTCTGGGCCT	CCATGGAATC	GCCCAGTAAT	2880
GACCTGGTCT	CCGGTGTGCC	TGTCGGAACC	CAGACCCGGA	GGTACCTTAG	CGGGTCATTA	
ACCCATGGTC	TCCATCGCTT	CCGGGGCATC	TTCAACTGGG	TGCTGAGCTA	TCGGCGTGAT	2940
TGGGTACCAG	AGGTAGCGAA	GGCCCCGTAG	AAGTTGACCC	ACGACTCGAT	AGCCGCACTA	
EcoRI	8850			8771		
TCAGATATCT	TTGTACCCTA	CGGTCGCTTG	GAGCCTCTCT	CTGGGCCCCAC	ATCCCCACTA	3000
AGTCTATAGA	AACATGGGAT	GCCAGCGAAC	CTCGGAGAGA	GACCCGGGTG	TAGGGGTGAT	
CCGGCCAAAA	GCAGGATGGC	TGCCTGGGTG	ATCAGCAATT	TCCAGGAGCG	GCAGCAGCGT	3060
GGCCGGTTTT	CGTCCTACCG	ACGGACCCAC	TAGTCGTAA	AGGTCCCTCGC	CGTCGTCGCA	
			PstI		8852	
GCAAAGCTGT	ACCGGCAGCT	GGCCCCTCAT	CTGCAGGTGG	ATGTGTTTCGG	TCGCGCCAGC	3120
CGTTTCGACA	TGGCCGTCGA	CCGGGGAGTA	GACGTCCACC	TACACAAGCC	AGCGCGGTGC	
GGACGGCCCC	TATGCGCTAA	TTGTCTGCTG	CCCACTTTGG	CCCGGTACCG	CTTCTACCTG	3180
CCTGCCGGGG	ATACGCGATT	AACAGACGAC	GGGTGAAACC	GGGCCATGGC	GAAGATGGAC	
	8714					
GCCTTTGAGA	ACTCACAGCA	TCGGGACTAC	ATCACTGAGA	AGTTCTGGCG	CAATGCCCTG	3240
CGGAAACTCT	TGAGTGTCGT	AGCCCTGATG	TAGTGACTCT	TCAAGACCGC	GTTACGGGAC	

EXHIBIT E

8715
GCGGCTGGTG CTGTACCCGT GCGGCTGGGA CCTCCTCGGG CCACCTACGA GGCTTTTGTG 3300
CGCCGACCAC GACATGGGCA CCGCGACCCCT GGAGGAGCCC GGTGGATGCT CCGAAAACAC

8715 8848
CCACCAGATG CCTTTGTACA CGTGGACGAC TTCAGCTCTG CCCGTGAACT **GGCTGTCTTC** 3360
GGTGGTCTAC GGAAACATGT GCACCTGCTG AAGTCGAGAC GGGCACTTGA CCGACAGAAG

CTCGTCAGCA TGAATGAGAG TCGTTATCGT GGCTTCTTTG CTTGGCGAGA CCGGCTCCGT 3420
GAGCAGTCGT **ACTTACTCTC** **AGCAATAGCA** CCGAAGAAAC GAACCGCTCT GCGCGAGGCA

8868 8849
GTGCGGCTCC TGGGTGACTG **GAGGGAGCGC** **TTCTGCACCA** TCTGTGCCCCG CTACCCCTTAC 3480
CACGCCGAGG ACCCACTGAC CTCCCTCGCG AAGACGTGGT AGACACGGGC **GATGGGAATG**

Stop codon 8876
TTGCCCCGCA GCCAGGTCTA TGAAGACCTT GAAAGCTGGT TCCAGGCTTG **AACTCCTGCT** 3540
AACGGGGCGT CGGTCCAGAT **ACTTCTGGAA** **CTTTTCGACCA** **AGGTCCGAAC** TTCAGGACGA

625B
GCTGGGAGAG GCTGGATGGG TGGGAGACTG ATGTTGAAAC CAAAGAGCTG GGCATCCAGG 3600
CGACCCTCTC CGACCTACCC ACCCTCTGAC TACAACCTTG GTTTCTCGAC CCGTAGGTCC

8905 EcoRI
CTTTTGGTCA CCATGGCACT ACCCCAAGGC TTTTCCTGTT CAGTGAGCAG **GAATTCAGGA** 3660
GAAAACCACT **GGTACCGTCA** TGGGGTTCCG AAAAGGACAA GTCACCTCTC **CTTAAGTCCT**

8877
TATAAGGAGA AAAGTGGGCT GAGATGCCCT GGTGGGCTTT AGAGTAGGGG CCCAGGATAA 3720
ATATTCTCTT TTTGACCCGA CTCTACGGGA CCACCCGAAA TCTCATCCCC GGGTCTCTATT

GAGACAATGA ATTAATGAGG AGCATATGGG GAAGGTGGCT GAGGGTCCCT GACTTACCTT 3780
CTCTGTTACT TAATTACTCC TCGTATACCC CTTCCACCGA CTCCCAGGGA CTGAATGGAA

GACCCATGGC TGAAGGCTCC ATGCCCATGG CTGGAGCTGG GACCCTACAC TTCTATAGTC 3840
CTGGGTACCG ACTTCCGAGG TACGGGTACC GACCTCGACC CTGGGATGTG AAGATATCAG

8954
AAGGTGCTTA GCCTCAAGGT **TGCAGATGCA** **CCCTCTAGTA** CTCTGGGTGC AGACTGTACA 3900
TTCCACGAAT CGGAGTTCCA **ACGTCTACGT** **GGGAGATCAT** GAGACCCACG TCTGACATGT

8967
CTGGGCGCAG GGGGTTGTGG AAGGACAGTG CAGATGATTC TGGGCTTTTG ACACCACAGT 3960
GACCCGCGTC CCCCAACACC TTCCTGTCAC GTCTACTAAG ACCCGAAAAC TGTGGTGTCA

End of cDNA (G, bold and underlined)
TCCCCAGGG AAAGAGGCAC TACTAATAAA AACACTGACA GAAATCTCCT GGTCAAGTCT 4020
AGGGGGTCCC TTTCTCCGTG ATGATTATTT TTGTGACTGT **CTTTAGAGGA** CCAGTTCAGA

SacI
GTTAGGCAGC **AGAGCTCACC** AGCCAGCTTC CTCTGCTCAA TTCCCTCCGG CAGCCATTAT 4080
CAATCCGTCG **TCTCGAGTGG** TCGGTCGAA GAGACGAGTT AAGGGAGGCC GTCGGTAATA

TGGGTTTCTC GTTTCTGTCT GAGAGCCTTG CTTGAGTGGT ACCTTACCAG GAACTCAAAG 4140
ACCCAAAGAC CAAAGACAGA **CTCTCGGAAC** **GAACTCACCA** TGGAATGGTC CTTGAGTTTC

8713
CCCACGGCAG GTACAGACCT GAGAACTGAG GTCAGACACA GCTGTGGCTG AGGTGCCACA 4200
GGGTGCCGTC CATGTCTGGA CTCTTGACTC CAGTCTGTGT CGACACCGAC TCCACGGTGT

TGTCATAGGT CTCAGTGGGA GGTGTGTCCCT GTGTGATGGG GTGTGATGTA TCCGTTAGGG 4260
ACAGTATCCA GAGTCACCCCT CCACACAGGA CACACTACCC CACACTACAT AGGCAATCCC

PstI
CTTTCACTGA AGAGCCTGCT **GCAGGTGCC** ACTGTGTTGG ACTGGGTGGG CCAGGAGGAG 4320
GAAAGTGACT TCTCGGACGA **CGTCCACGGG** TGACACAACC TGACCCACCC GGTCTCTCTC

ATGAGAGGTG AGGCTATGAG TGTATGACAG ATTGAGCTCC TGGGATGGGC TGGGGCTTGG 4380
TACTCTCCAC TCCGATACTC ACATACTGTC TAACTCGAGG ACCCTACCCG ACCCCGAACC

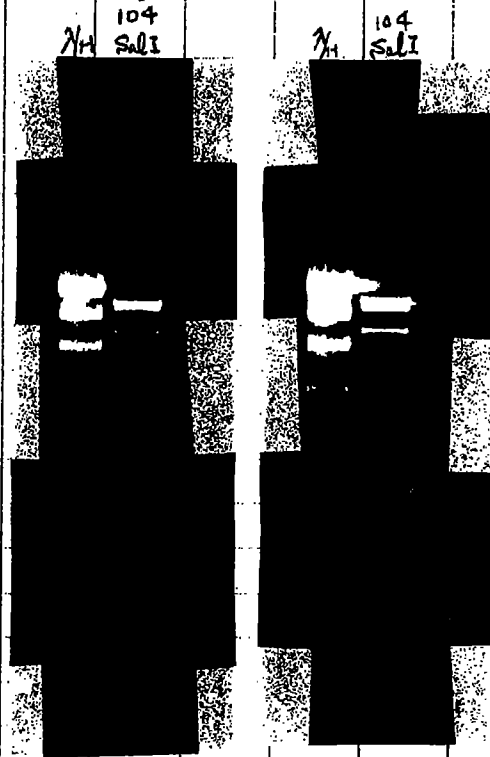
EXHIBIT E

GTTTGTCCGG GGATGGGGTG GCAGTACAGG CAGGAAGCTG CCCTCCCCCT GTGGTTTGTG 4440
CAAACAGGCC CCTACCCAC CGTCATGTCC GTCCTTCGAC GGGAGGGGGA CACCAAACAC

GGAAAGGCCT AACCATGGCT TCCTGCCCTA ATCTAGCCTC ATGGG 4485
CCTTTCCGGA TTGGTACCGA AGGACGGGAT TAGATCGGAG TACCC

Southern blot of mFT7 phage (104)

1 μ l 104 phage (~0.75 μ g)
 ↓ Sal I digest
 ↓ 0.6 % agarose GE



© No Sal I site in insert DNA of 104-phage

20kb arm	Sal	insert	Sal	20kb arm	λ -FIX II
----------	-----	--------	-----	----------	-------------------

ea. 1 μ l 104 phage (~0.75 μ g)
 ↓ EcoRI or Pst I digest
 ↓ conc. of NaCl adjust to 150 mM
 ↓ Sal I digest 0.1%

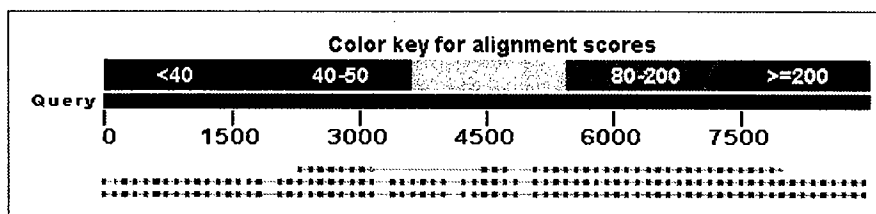
ea. 7.5 μ l FVB mouse gDNA (15 μ g)
 ↓ EcoRI or Pst I digest 0.1%

BLAST Basic Local Alignment Search ToolJob Title: lcl|32071 (8970 letters)

•
•
•**BLASTN 2.2.17 (Aug-26-2007)**RID: HB3E8W8B013 **Database:** mouse build 37 RNA, reference and alternate assemblies 53,645 sequences;
5,338,491,926 total letters**Genome View**Show positions of the BLAST hits in the house mouse genome using the Entrez
Genomes MapViewer

Query= Length=8970

Distribution of 178 Blast Hits on the Query Sequence

**Exhibit G**

[Distance tree of results](#) **NEW**Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map Viewer**Sequences producing significant alignments:**

(Click headers to sort columns)

Transcripts

NM_013524.2	Mus musculus fucosyltransferase 7 (Fut7), mRNA	117	3969	23%	2e-22	100%	U E G M
--------------------	--	-----	------	-----	-------	------	--------------------------

Genomic sequences [show first]

NW_001030686.1	Mus musculus chromosome 2 genomic contig, alternate assembly (based on Celera assembly)	121	7907	47%	2e-23	100%
NT_039206.7	Mus musculus chromosome 2 genomic contig, strain C57BL/6J	121	7962	48%	2e-23	100%



PubMed

Nucleotide

Protein

Genome

Structure

PMC

Taxonomy

OMIM

My NCBI

[\[Sign In\]](#)[\[Register\]](#)

Books

Search Nucleotide

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display GenBank

Show 5

Send to

Hide: ☐sequence ☐

all but gene, CDS and mRNA features

Range: from begin

to end

☐ Reverse complemented strand

Features:

☒ STS☒ Exon

+

Refresh

☐ 1: NM_013524. Reports Mus musculus fuco...[gi:118129912][Links](#)[Comment](#) [Features](#) [Sequence](#)

LOCUS NM_013524 2185 bp mRNA linear ROD 03-SEP-2007

DEFINITION Mus musculus fucosyltransferase 7 (Fut7), mRNA.

ACCESSION NM_013524

VERSION NM_013524.2 GI:118129912

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2185)

AUTHORS Hiraoka,N., Petryniak,B., Kawashima,H., Mitoma,J., Akama,T.O., Fukuda,M.N., Lowe,J.B. and Fukuda,M.

TITLE Significant decrease in alpha1,3-linked fucose in association with increase in 6-sulfated N-acetylglucosamine in peripheral lymph node addressin of FucT-VII-deficient mice exhibiting diminished lymphocyte homing

JOURNAL Glycobiology 17 (3), 277-293 (2007)

PUBMED 17172261

REMARK GeneRIF: Keratan sulfate sulfotransferase competes with FucT-VII for the same acceptor substrate and downregulates the synthesis of L-selectin ligand by inhibiting alpha1,3-fucosylation.

REFERENCE 2 (bases 1 to 2185)

AUTHORS Laubli,H., Stevenson,J.L., Varki,A., Varki,N.M. and Borsig,L.

TITLE L-selectin facilitation of metastasis involves temporal induction of Fut7-dependent ligands at sites of tumor cell arrest

JOURNAL Cancer Res. 66 (3), 1536-1542 (2006)

PUBMED 16452210

REFERENCE 3 (bases 1 to 2185)

AUTHORS Chen,S., Kawashima,H., Lowe,J.B., Lanier,L.L. and Fukuda,M.

TITLE Suppression of tumor formation in lymph nodes by L-selectin-mediated natural killer cell recruitment

JOURNAL J. Exp. Med. 202 (12), 1679-1689 (2005)

PUBMED 16352740

REFERENCE 4 (bases 1 to 2185)

AUTHORS Eom,H.S., Rubio,M.T., Means,T.K., Luster,A.D. and Sykes,M.

TITLE T-cell P/E-selectin ligand alpha(1,3)fucosylation is not required for graft-vs-host disease induction

JOURNAL Exp. Hematol. 33 (12), 1564-1573 (2005)

PUBMED 16338500

REFERENCE 5 (bases 1 to 2185)

AUTHORS Satoh,T., Kanai,Y., Wu,M.H., Yokozeki,H., Kannagi,R., Lowe,J.B. and Nishioka,K.

TITLE Synthesis of {alpha}(1,3) fucosyltransferases IV- and VII-dependent eosinophil selectin ligand and recruitment to the skin

JOURNAL Am. J. Pathol. 167 (3), 787-796 (2005)

PUBMED 16127157

REMARK GeneRIF: FT-IV and FT-VII are both important contributors to selectin-dependent eosinophil recruitment to the skin and may represent therapeutic targets for treating diseases in which eosinophil recruitment contributes to pathophysiology.

REFERENCE 6 (bases 1 to 2185)
 AUTHORS Homeister,J.W., Thall,A.D., Petryniak,B., Maly,P., Rogers,C.E.,
 Smith,P.L., Kelly,R.J., Gersten,K.M., Askari,S.W., Cheng,G.,
 Smithson,G., Marks,R.M., Misra,A.K., Hinds Gaul,O., von Andrian,U.H.
 and Lowe,J.B.
 TITLE The alpha(1,3)fucosyltransferases FucT-IV and FucT-VII exert
 collaborative control over selectin-dependent leukocyte recruitment
 and lymphocyte homing
 JOURNAL Immunity 15 (1), 115-126 (2001)
 PUBMED [11485743](#)

REFERENCE 7 (bases 1 to 2185)
 AUTHORS Beck,P.L., Xavier,R., Lu,N., Nanda,N.N., Dinauer,M., Podolsky,D.K.
 and Seed,B.
 TITLE Mechanisms of NSAID-induced gastrointestinal injury defined using
 mutant mice
 JOURNAL Gastroenterology 119 (3), 699-705 (2000)
 PUBMED [10982764](#)

REFERENCE 8 (bases 1 to 2185)
 AUTHORS Weninger,W., Ulfman,L.H., Cheng,G., Souchkova,N., Quackenbush,E.J.,
 Lowe,J.B. and von Andrian,U.H.
 TITLE Specialized contributions by alpha(1,3)-fucosyltransferase-IV and
 FucT-VII during leukocyte rolling in dermal microvessels
 JOURNAL Immunity 12 (6), 665-676 (2000)
 PUBMED [10894166](#)

REFERENCE 9 (bases 1 to 2185)
 AUTHORS Maly,P., Thall,A., Petryniak,B., Rogers,C.E., Smith,P.L.,
 Marks,R.M., Kelly,R.J., Gersten,K.M., Cheng,G., Saunders,T.L.,
 Camper,S.A., Camphausen,R.T., Sullivan,F.X., Isogai,Y.,
 Hinds Gaul,O., von Andrian,U.H. and Lowe,J.B.
 TITLE The alpha(1,3)fucosyltransferase Fuc-TVII controls leukocyte
 trafficking through an essential role in L-, E-, and P-selectin
 ligand biosynthesis
 JOURNAL Cell 86 (4), 643-653 (1996)
 PUBMED [8752218](#)

REFERENCE 10 (bases 1 to 2185)
 AUTHORS Smith,P.L., Gersten,K.M., Petryniak,B., Kelly,R.J., Rogers,C.,
 Natsuka,Y., Alford,J.A. III, Scheidegger,E.P., Natsuka,S. and
 Lowe,J.B.
 TITLE Expression of the alpha(1,3)fucosyltransferase Fuc-TVII in lymphoid
 aggregate high endothelial venules correlates with expression of
 L-selectin ligands
 JOURNAL J. Biol. Chem. 271 (14), 8250-8259 (1996)
 PUBMED [8626519](#)

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from [AL732557.4](#).
 On Nov 17, 2006 this sequence version replaced [gi:7305072](#).

Sequence Note: The RefSeq transcript and protein were derived from
 genomic sequence to make the sequence consistent with the reference
 genome assembly. The genomic coordinates used for the transcript
 record were based on alignments.

Publication Note: This RefSeq record includes a subset of the
 publications that are available for this gene. Please see the
 Entrez Gene record to access additional publications.

PRIMARY	REFSEQ_SPAN	PRIMARY_IDENTIFIER	PRIMARY_SPAN	COMP
	1-13	AL732557.4	96057-96069	
	14-493	AL732557.4	96262-96741	
	494-699	AL732557.4	97346-97551	
	700-2185	AL732557.4	97659-99144	

FEATURES

source

Location/Qualifiers

1..2185

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/chromosome="2"

gene

1..2185

```

/gene="Fut7"
/note="fucosyltransferase 7; synonyms: FTVII, AI853193,
Fuc-TVII, FucT-VII, MGC124225"
/db_xref="GeneID:14347"
/db_xref="MGI:107692"
exon 1..13
/gene="Fut7"
/inference="alignment:Splign"
/number=1
exon 14..493
/gene="Fut7"
/inference="alignment:Splign"
/number=2
STS 255..1881
/gene="Fut7"
/db_xref="UniSTS:489188"
exon 494..699
/gene="Fut7"
/inference="alignment:Splign"
/number=3
CDS 687..1715
/gene="Fut7"
/GO_component="integral to membrane; membrane"
/GO_function="fucosyltransferase activity; transferase
activity; transferase activity, transferring glycosyl
groups"
/GO_process="protein amino acid glycosylation"
/codon_start=1
/product="fucosyltransferase 7"
/protein_id="NP_038552.1"
/db_xref="GI:7305073"
/db_xref="CCDS:CCDS15772.1"
/db_xref="GeneID:14347"
/db_xref="MGI:107692"
/translation="MNCIGYHPTRRLRAWGGLAGGATFMVIWFFWLWGSAPGSAPVPQ
STLTILIIWHWPFTNRPELPGDTC TRYGMASCRSLSANRSLASADAVVFHRELQTRQ
SLLPLDQRP HQPWVWASMEPSNTHGLHRFRGIFNWVLSYRRSDIFVPYGRLEPLS
GPTSPLPAKSRMAAWVISNFQERQQRALYRQLAPHLQVDVFGRASGRPLCANCLLPT
LARYRFYLAFENSQHRDYITEKFWRNALAAGAVPVALGPPRATYEA FVPPDAFVHVDD
FSSARELAVFLVSMNESRYRGFFAWRDRLRVLLGDWRERFCTICARYPYLPRSQVYE
DLESWFQA"
exon 700..2185
/gene="Fut7"
/inference="alignment:Splign"
/number=4
STS 1849..1969
/gene="Fut7"
/standard_name="AI853193"
/db_xref="UniSTS:178581"
STS 1870..2043
/gene="Fut7"
/db_xref="UniSTS:224625"
polyA_signal 2169..2174
/gene="Fut7"

```

ORIGIN

```

1 ccatggcact gctccagtct ggagctctgg gacatggaca agccaggcct gctattctcc
61 atacagggct ccatagtgtc tggtcagca gagtggggga tctggtgggg atggaggaag
121 cttagctaaa agctttgtat aggctgaagc tctgagtga cctgctgggc caccctaccc
181 tgggtctgggc tgggtcattg catccccaga ttggaaggct tggtgagatg gagaggaacc
241 ttggctacaa gctatagctt tgcccaccag agcctgctgg aggggaatca aacaagcctg
301 gacctgaggc tgggactagc ttctctgttt ctggagtggg tgccaacccc ctgcccacca
361 gcctgcctgt ccacgccagg gacacacaga ctccctccct ttccagactg gaaagccccc
421 tcctgggaga gcaggaagga agcaacctgc aactcttcca gccctggacc ttgggctgaa
481 cctacagttc aagtgggtga tgccaaagat tgaaggggta ggcggggca gaagtgggaa
541 ggtccctggc ttctcacct tggtagatgg tgaggagccc cagagggtta gctgagcagc
601 agctgtgatt tcagggtgcc tctgttgag aggctgctgt gatttgaaaa tcttctttcc
661 ttggtgacaa ttccagaagg ctccagatga attgtattgg gtaccacccc accaggaggc
721 tgcgggcctg ggcggccta gctggaggag caacattcat ggtaatttgg tttttctggc

```

```
781 tgtggggatc agctcctgga agtgcccctg tgccctcagtc cacactcacc atccttatct
841 ggcaactggcc ttccaccaac cggccgcccag agctacctgg tgacacctgc actcgctatg
901 gcatggccag ctgccgtctg agtgctaacc ggagcctgct agccagtgct gatgctgtgg
961 tcttccacca ccgtgagctg caaaccgggc aatctctcct acccctggac cagaggccac
1021 acggacagcc ttgggtcttg gcctccatgg aatcgcccag taatacccat ggtctccatc
1081 gcttccgggg catcttcaac tgggtgctga gctatcggcg tgattcagat atctttgtac
1141 cctacgggtcg cttggagcct ctctctgggc ccacatcccc actaccggcc aaaagcagga
1201 tggctgcctg ggtgatcagc aatttccagg agcggcagca gcgtgcaaag ctgtaccggc
1261 agctggcccc tcatctgcag gtggatgtgt tcggtcgcgc cagcggacgg cccctatgcg
1321 ctaattgtct gctgccact ttggcccgtt accgcttcta cctggccttt gagaactcac
1381 agcatcggga ctacatcact gagaagttct ggcgcaatgc cctggcggct ggtgctgtac
1441 ccgtggcgct gggacctcct cgggccacct acgaggcttt tgtgccacca gatgcctttg
1501 tacacgtgga cgacttcagc tctgcccggt aactggctgt ctctctcgtc agcatgaatg
1561 agagtcgtta tcgtggcttc tttgcttggc gagaccggct ccgtgtgcgg ctccctgggtg
1621 actggaggga gcgcttctgc accatctgtg cccgctacct ttacttgccc cgcagccagg
1681 tctatgaaga ccttgaagc tggttccagg cttgaactcc tgctgctggg agaggctgga
1741 tgggtgggag actgatgttg aaaccaaaga gctgggcata caggcttttg gtcaccatgg
1801 cactacccca aggcttttcc tgttcagtga gcaggaaatc aggatataag gagaaaactg
1861 ggctgagatg ccctgggtgg ctttagagta ggggcccagg ataagagaca atgaattaat
1921 gagagcata tggggaaggt ggctgaggt ccctgactta ccttgacca tggctgaagg
1981 ctccatgccc atggctggag ctgggaccct acacttctat agtcaagggt cttagcctca
2041 aggttgcaga tgcaccctct agtactctgg gtgcagactg tacactgggc gcagggggtt
2101 gtggaaggac agtgcagatg attctgggct tttgacacca cagttcccc agggaaagag
2161 gcactactaa taaaacact gacag
```

//

[Disclaimer](#) | [Write to the Help Desk](#)
[NCBI](#) | [NLM](#) | [NIH](#)

Aug 28 2007 16:53:42



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)**BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]**

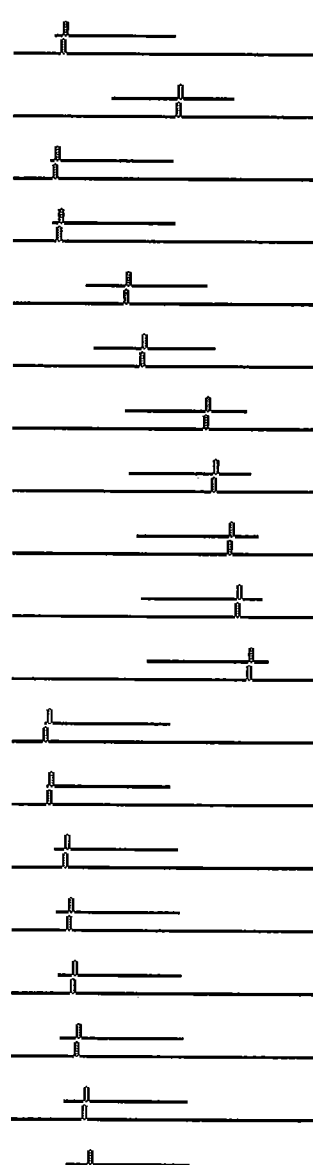
Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x_dropoff: 0 expect: 10.000 wordsize: 11 Filter ☐ View option: Standard
Masking character option X for protein, n for nucleotide Masking color option Black
☐ Show CDS translation

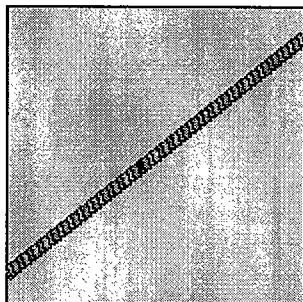
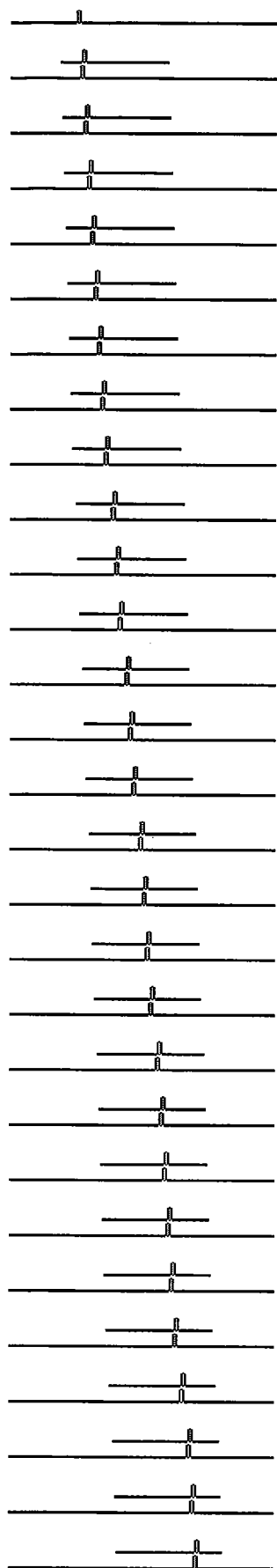
Sequence 1: lcl|1
Length = 3594 (1 .. 3594)

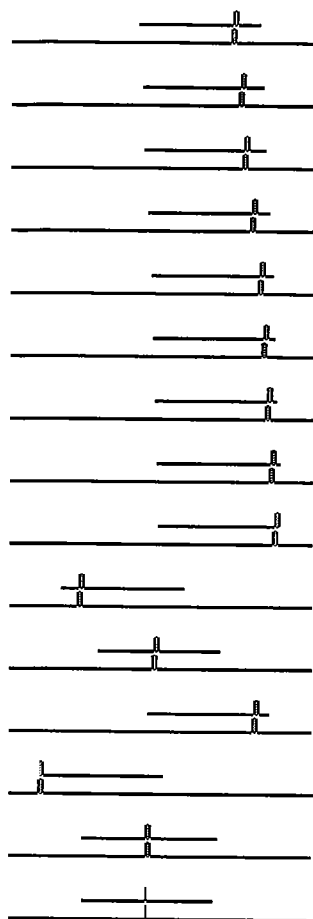
SEQ ID NO:1

Sequence 2: lcl|65536
Length = 8970 (1 .. 8970)

PHAGE 104







1

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

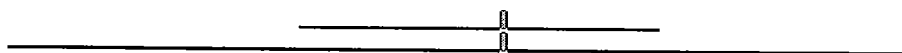
NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 125 bits (65), Expect = 1e-24
Identities = 65/65 (100%), Gaps = 0/65 (0%)
Strand=Plus/Plus

```
Query 272 TACCGCTGCCCACCTCGTGCCACCTTACGTTATACCTCAAACCAGCTAGATAGTTTCTG 331
          |||
Sbjct 1441 TACCGCTGCCCACCTCGTGCCACCTTACGTTATACCTCAAACCAGCTAGATAGTTTCTG 1500

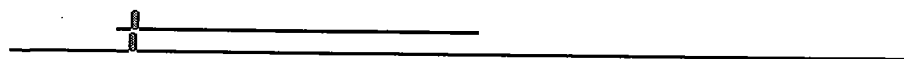
Query 332 ATGGC 336
          ||||
Sbjct 1501 ATGGC 1505
```



Score = 121 bits (63), Expect = 2e-23
Identities = 63/63 (100%), Gaps = 0/63 (0%)
Strand=Plus/Plus

```
Query 2012 GTGTCCCTGAGCCTAGGGTGACAGGCCTCTCCTTTTTTTTATCTGCTTCAGGGTAC 2071
          |||
Sbjct 4921 GTGTCCCTGAGCCTAGGGTGACAGGCCTCTCCTTTTTTTTATCTGCTTCAGGGTAC 4980
```

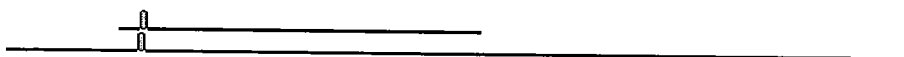
Query 2072 CAC 2074
|||
Sbjct 4981 CAC 4983



Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

Query 152 TGTGACTCTCCTGGGGTCACCAGCTTGGGGAGAGGTGAAGAAAGATGCCGGGGCGGAAAC 211
|||||
Sbjct 1201 TGTGACTCTCCTGGGGTCACCAGCTTGGGGAGAGGTGAAGAAAGATGCCGGGGCGGAAAC 1260

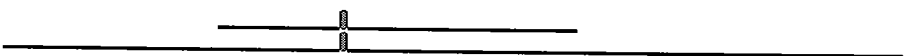
Query 212 A 212
|
Sbjct 1261 A 1261



Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

Query 212 AAAGGGGCAGATATCACTATGGTTATCTTACTAAGCACAGAGTAACTGAAAAAGCAAGGG 271
|||||
Sbjct 1321 AAAGGGGCAGATATCACTATGGTTATCTTACTAAGCACAGAGTAACTGAAAAAGCAAGGG 1380

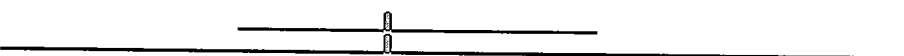
Query 272 T 272
|
Sbjct 1381 T 1381



Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

Query 1232 AGCTCCTGGGTCTGCCCTTCAGGGCAAGTGCTGACGCTCCATCAGACTGTGATGGGGCCC 1291
|||||
Sbjct 3361 AGCTCCTGGGTCTGCCCTTCAGGGCAAGTGCTGACGCTCCATCAGACTGTGATGGGGCCC 3420

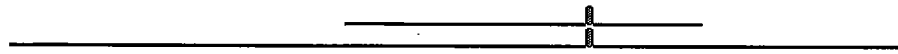
Query 1292 T 1292
|
Sbjct 3421 T 3421



Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

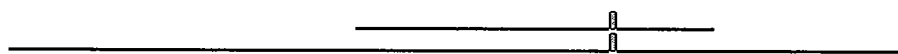
Query 1472 GGGTGGCCTGGGGTTGTGTGGTGGGCAGAGGACGGAGGTGCTCATTGGGGGAAGGGATCA 1531
|||||

Sbjct 3841 GGGTGGCCTGGGGTGTGTGGTGGGCAGAGGACGGAGGTGCTCATTGGGGGAAGGGATCA 3900
Query 1532 C 1532
|
Sbjct 3901 C 3901



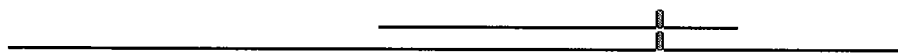
Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

Query 2432 ACCCATGGTCTCCATCGCTTCCGGGGCATCTTCAACTGGGTGCTGAGCTATCGGCGTGAT 2491
|
Sbjct 5761 ACCCATGGTCTCCATCGCTTCCGGGGCATCTTCAACTGGGTGCTGAGCTATCGGCGTGAT 5820
Query 2492 T 2492
|
Sbjct 5821 T 5821



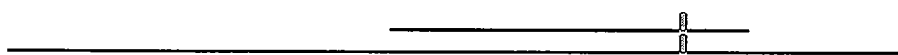
Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

Query 2552 CCGGCCAAAAGCAGGATGGCTGCCTGGGTGATCAGCAATTTCCAGGAGCGGCAGCAGCGT 2611
|
Sbjct 6001 CCGGCCAAAAGCAGGATGGCTGCCTGGGTGATCAGCAATTTCCAGGAGCGGCAGCAGCGT 6060
Query 2612 G 2612
|
Sbjct 6061 G 6061



Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

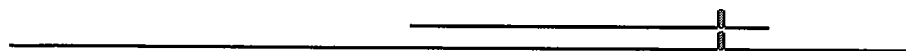
Query 2792 GCGGCTGGTGTGTACCCGTGGCGCTGGGACCTCCTCGGGCCACCTACGAGGCTTTTGTG 2851
|
Sbjct 6481 GCGGCTGGTGTGTACCCGTGGCGCTGGGACCTCCTCGGGCCACCTACGAGGCTTTTGTG 6540
Query 2852 C 2852
|
Sbjct 6541 C 6541



Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

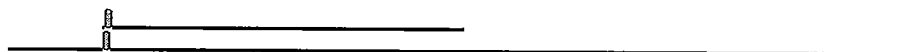
Query 2912 CTCGTCAGCATGAATGAGAGTCGTTATCGTGGCTTCTTTGCTTGGCGAGACCGGCTCCGT 2971

Sbjct 6721 |||||CTCGTCAGCATGAATGAGAGTCGTTATCGTGGCTTCTTTGCTTGGCGAGACCGGCTCCGT 6780
Query 2972 G 2972
|
Sbjct 6781 G 6781



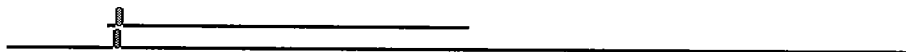
Score = 117 bits (61), Expect = 2e-22
Identities = 61/61 (100%), Gaps = 0/61 (0%)
Strand=Plus/Plus

Query 3092 GCTGGGAGAGGCTGGATGGGTGGGAGACTGATGTTGAAACCAAAGAGCTGGGCATCCAGG 3151
|||||
Sbjct 7081 GCTGGGAGAGGCTGGATGGGTGGGAGACTGATGTTGAAACCAAAGAGCTGGGCATCCAGG 7140
Query 3152 C 3152
|
Sbjct 7141 C 7141



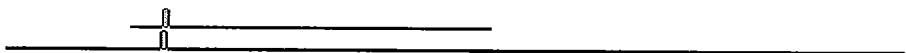
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 32 CAGAAGCCTGTGGCCCCAAGCTGGCAGGATGGCCCCCTTCCTGCAGGTCCCCACAGCCT 91
|||||
Sbjct 961 CAGAAGCCTGTGGCCCCAAGCTGGCAGGATGGCCCCCTTCCTGCAGGTCCCCACAGCCT 1020



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 92 TCTGGGTTCTTGACACGAGAGAAGAGGTGGGGCGGGGTGAAGTGAACCTGAAGCCAAAA 151
|||||
Sbjct 1081 TCTGGGTTCTTGACACGAGAGAAGAGGTGGGGCGGGGTGAAGTGAACCTGAAGCCAAAA 1140



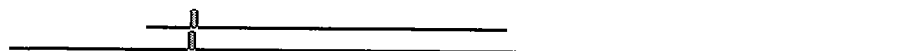
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 332 ATGGCACCCATACCCTCCCTTCCCTTTAGGCATTGCGCAAGCTCTCCACCACAATCTGG 391
|||||
Sbjct 1561 ATGGCACCCATACCCTCCCTTCCCTTTAGGCATTGCGCAAGCTCTCCACCACAATCTGG 1620



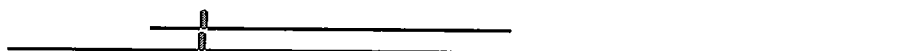
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 392 AAGTTATACCCTGCGAGGGGATGGGCAGGGCACTTCTGAGGTGCCAATCAGCCTGCACTC 451
|||||
Sbjct 1681 AAGTTATACCCTGCGAGGGGATGGGCAGGGCACTTCTGAGGTGCCAATCAGCCTGCACTC 1740



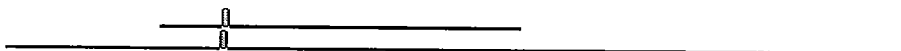
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 452 GCCTCTGCCCTGGCCATGGCACTGCTGTCAGTTTCTTGGTACCTGTCTCAACAGCAGCCT 511
|||||
Sbjct 1801 GCCTCTGCCCTGGCCATGGCACTGCTGTCAGTTTCTTGGTACCTGTCTCAACAGCAGCCT 1860



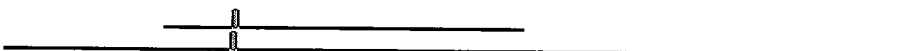
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 512 TGTCACGTGAGACTATGGCTGGCGGTGGGGGTGGGGGCAGGAATCCTAGAACACAGGAG 571
|||||
Sbjct 1921 TGTCACGTGAGACTATGGCTGGCGGTGGGGGTGGGGGCAGGAATCCTAGAACACAGGAG 1980



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 632 GGACGATCTGGCCAACACTGTCTCTCCATTCAAACCTCCAGTCTGGAGCTCTGGGACAT 691
|||||
Sbjct 2161 GGACGATCTGGCCAACACTGTCTCTCCATTCAAACCTCCAGTCTGGAGCTCTGGGACAT 2220



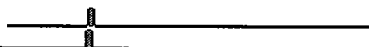
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 692 GGACAAGCCAGGCCTGCTATTCTCCATACAGGGCTCCATAGTGTCTGGCTCAGCAGAGTG 751
|||||
Sbjct 2281 GGACAAGCCAGGCCTGCTATTCTCCATACAGGGCTCCATAGTGTCTGGCTCAGCAGAGTG 2340



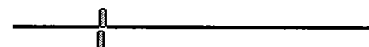
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 752 GGGGATCTGGTGGGGATGGAGGAAGCTTAGCTAAAAGCTTTGTATAGGCTGAAGCTCTGA 811
|||||
Sbjct 2401 GGGGATCTGGTGGGGATGGAGGAAGCTTAGCTAAAAGCTTTGTATAGGCTGAAGCTCTGA 2460



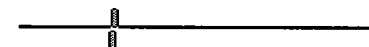
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 812 GTGACCCCTGCTGGGCCACCCCTACCCTGGTCTGGGCTGGGTCATTGCATCCCCAGATTGGA 871
|||||
Sbjct 2521 GTGACCCCTGCTGGGCCACCCCTACCCTGGTCTGGGCTGGGTCATTGCATCCCCAGATTGGA 2580



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 872 AGGCTTGGTGAGATGGAGAGGAACCTTGGCTACAAGCTATAGCTTTGCCACCCAGAGCCT 931
|||||
Sbjct 2641 AGGCTTGGTGAGATGGAGAGGAACCTTGGCTACAAGCTATAGCTTTGCCACCCAGAGCCT 2700



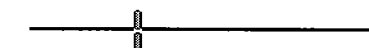
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 932 GCTGGAGGGGAATCAAACAAGCCTGGACCTGAGGCTGGGACTAGCTTTCCTGTTTCTGGA 991
|||||
Sbjct 2761 GCTGGAGGGGAATCAAACAAGCCTGGACCTGAGGCTGGGACTAGCTTTCCTGTTTCTGGA 2820



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 992 GTGGATGCCAACCCCTGCCACACAGCCTGCCTGTCCAGCCAGGGACACACAGACTCCT 1051
|||||
Sbjct 2881 GTGGATGCCAACCCCTGCCACACAGCCTGCCTGTCCAGCCAGGGACACACAGACTCCT 2940



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1052 TCCCTTTCCAGACTGGAAAGCCCCCTCCTGGGAGAGCAGGAAGGAAGCAACCTGCAACTC 1111
|||||
Sbjct 3001 TCCCTTTCCAGACTGGAAAGCCCCCTCCTGGGAGAGCAGGAAGGAAGCAACCTGCAACTC 3060

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1112 TTCCAGCCCTGGACCTTGGGCTGAACCTACAGTTCAAGGTTTGTATGCTCACAGGTCTTG 1171
|||||
Sbjct 3121 TTCCAGCCCTGGACCTTGGGCTGAACCTACAGTTCAAGGTTTGTATGCTCACAGGTCTTG 3180

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1172 GCAGGGAAAGATAAGAATCCCCAGGGCACCTCCCCCGCCCCCAGTCCACTGCAGGT 1231
|||||
Sbjct 3241 GCAGGGAAAGATAAGAATCCCCAGGGCACCTCCCCCGCCCCCAGTCCACTGCAGGT 3300

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1292 TTTTCTGAGGATGACAATTCTGAGAACAAGGCATTTTCTAGAGGTGGCAGAACAGCATT 1351
|||||
Sbjct 3481 TTTTCTGAGGATGACAATTCTGAGAACAAGGCATTTTCTAGAGGTGGCAGAACAGCATT 3540

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1352 TTGTGATGCCCCGAGGATCTGGGAGCACAGGTCCAGCTTAATGAGGGATTGGAGGAAGTGG 1411
|||||
Sbjct 3601 TTGTGATGCCCCGAGGATCTGGGAGCACAGGTCCAGCTTAATGAGGGATTGGAGGAAGTGG 3660

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1412 GTATCATCATTACAGGGAGGGGCCTCTGTGGCCTCCTGGGAAAATGCAGTTGCTCTCTTT 1471
|||||
Sbjct 3721 GTATCATCATTACAGGGAGGGGCCTCTGTGGCCTCCTGGGAAAATGCAGTTGCTCTCTTT 3780

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1532 CTTCTGCTCAGAGTGCTCGCAAGGGCCTTTCCTTTTCCTGAAGGCAAGCAGGCCTCCTCC 1591
|||||
Sbjct 3961 CTTCTGCTCAGAGTGCTCGCAAGGGCCTTTCCTTTTCCTGAAGGCAAGCAGGCCTCCTCC 4020

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1592 TCCTCCTCTTCCTCCTTCTCCTCTTCCTCCTTTCTCCATATGCCTAGCTGGTCATTTC 1651
|||||
Sbjct 4081 TCCTCCTCTTCCTCCTTCTCCTCTTCCTCCTTTCTCCATATGCCTAGCTGGTCATTTC 4140

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

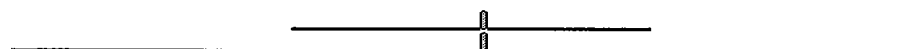
Query 1652 TAGGGACCAGCATGGTTGGGAAGGGGGCCTTGCTTGGCCTTCCTCTTGTCTCAATTCCC 1711
|||||
Sbjct 4201 TAGGGACCAGCATGGTTGGGAAGGGGGCCTTGCTTGGCCTTCCTCTTGTCTCAATTCCC 4260

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1772 GAAGGGGTAGGGCGGGGCAGAAGTGGGAAGGTCCTGGCTTCCTCACCTTGGTAGATGGT 1831
|||||
Sbjct 4441 GAAGGGGTAGGGCGGGGCAGAAGTGGGAAGGTCCTGGCTTCCTCACCTTGGTAGATGGT 4500

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1832 GAGGAGCCCCAGAGGTTGAGCTGAGCAGCAGCTGTGATTTCAGGGTGCCTCTGTTGGAGA 1891
|||||
Sbjct 4561 GAGGAGCCCCAGAGGTTGAGCTGAGCAGCAGCTGTGATTTCAGGGTGCCTCTGTTGGAGA 4620



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1892 GGCTGCTGTGATTGAAAATCTTCTTTCCTTGGTGACAATCCAGAAGGCTCCAGATGAA 1951
|||||
Sbjct 4681 GGCTGCTGTGATTGAAAATCTTCTTTCCTTGGTGACAATCCAGAAGGCTCCAGATGAA 4740



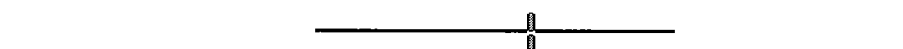
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 1952 TTGTATTGGTGAGTGCCTGGCCCTTAAGCAGTCCCAGCTGGGGATGATGGGGATTATGG 2011
|||||
Sbjct 4801 TTGTATTGGTGAGTGCCTGGCCCTTAAGCAGTCCCAGCTGGGGATGATGGGGATTATGG 4860



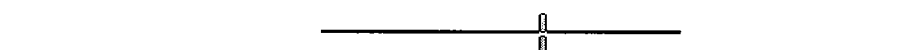
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2072 CACCCACACAGAGGCTGCGGGCCTGGGGCGGCCTAGCTGGAGGAGCAACATTCATGGTA 2131
|||||
Sbjct 5041 CACCCACACAGAGGCTGCGGGCCTGGGGCGGCCTAGCTGGAGGAGCAACATTCATGGTA 5100



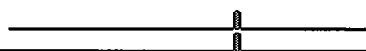
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2132 ATTTGGTTTTTCTGGCTGTGGGGATCAGCTCCTGGAAGTGCCCTGTGCCTCAGTCCACA 2191
|||||
Sbjct 5161 ATTTGGTTTTTCTGGCTGTGGGGATCAGCTCCTGGAAGTGCCCTGTGCCTCAGTCCACA 5220



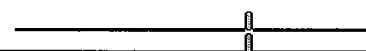
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2192 CTCACCATCCTTATCTGGCACTGGCCTTTCACCAACCGGCCGCCAGAGCTACCTGGTGAC 2251
|||||
Sbjct 5281 CTCACCATCCTTATCTGGCACTGGCCTTTCACCAACCGGCCGCCAGAGCTACCTGGTGAC 5340



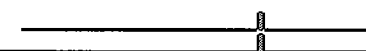
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2252 ACCTGCACTCGCTATGGCATGGCCAGCTGCCGTCTGAGTGCTAACCGGAGCCTGCTAGCC 2311
|||||
Sbjct 5401 ACCTGCACTCGCTATGGCATGGCCAGCTGCCGTCTGAGTGCTAACCGGAGCCTGCTAGCC 5460



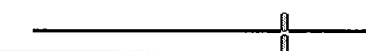
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2312 AGTGCTGATGCTGTGGTCTTCCACCACCGTGAGCTGCAAACCGGCAATCTCTCCTACCC 2371
|||||
Sbjct 5521 AGTGCTGATGCTGTGGTCTTCCACCACCGTGAGCTGCAAACCGGCAATCTCTCCTACCC 5580



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2372 CTGGACCAGAGGCCACACGGACAGCCTTGGGTCTGGGCCTCCATGGAATCGCCCAGTAAT 2431
|||||
Sbjct 5641 CTGGACCAGAGGCCACACGGACAGCCTTGGGTCTGGGCCTCCATGGAATCGCCCAGTAAT 5700



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2492 TCAGATATCTTTGTACCCTACGGTCGCTTGGAGCCTCTCTCTGGGCCCACATCCCCACTA 2551
|||||
Sbjct 5881 TCAGATATCTTTGTACCCTACGGTCGCTTGGAGCCTCTCTCTGGGCCCACATCCCCACTA 5940



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2612 GCAAAGCTGTACCGGCAGCTGGCCCCTCATCTGCAGGTGGATGTGTTTCGGTCGCGCCAGC 2671
|||||
Sbjct 6121 GCAAAGCTGTACCGGCAGCTGGCCCCTCATCTGCAGGTGGATGTGTTTCGGTCGCGCCAGC 6180

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2672 GGACGGCCCCCTATGCGCTAATTGTCTGCTGCCCACTTTGGCCCGGTACCGCTTCTACCTG 2731
|||||
Sbjct 6241 GGACGGCCCCCTATGCGCTAATTGTCTGCTGCCCACTTTGGCCCGGTACCGCTTCTACCTG 6300

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2732 GCCTTTGAGAACTCACAGCATCGGGACTACATCACTGAGAAGTTCTGGCGCAATGCCCTG 2791
|||||
Sbjct 6361 GCCTTTGAGAACTCACAGCATCGGGACTACATCACTGAGAAGTTCTGGCGCAATGCCCTG 6420

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

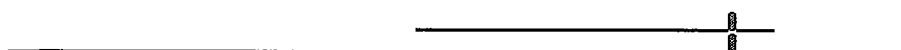
Query 2852 CCACCAGATGCCTTTGTACACGTGGACGACTTCAGCTCTGCCCGTGAAGTGGCTGTCTTC 2911
|||||
Sbjct 6601 CCACCAGATGCCTTTGTACACGTGGACGACTTCAGCTCTGCCCGTGAAGTGGCTGTCTTC 6660

Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 2972 GTGCGGCTCCTGGGTGACTGGAGGGAGCGCTTCTGCACCATCTGTGCCCGCTACCCCTAC 3031
|||||
Sbjct 6841 GTGCGGCTCCTGGGTGACTGGAGGGAGCGCTTCTGCACCATCTGTGCCCGCTACCCCTAC 6900

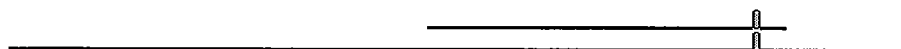
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 3032 TTGCCCCGAGCCAGGTCTATGAAGACCTTGAAAGCTGGTTCAGGCTTGAACCTCTGCT 3091
|||||
Sbjct 6961 TTGCCCCGAGCCAGGTCTATGAAGACCTTGAAAGCTGGTTCAGGCTTGAACCTCTGCT 7020



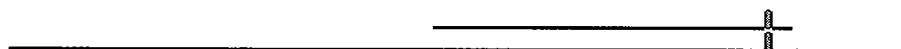
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 3152 CTTTGGTCACCATGGCACTACCCCAAGGCTTTTCCTGTTCAAGTGGAGCAGGAATTCAGGA 3211
|||||
Sbjct 7201 CTTTGGTCACCATGGCACTACCCCAAGGCTTTTCCTGTTCAAGTGGAGCAGGAATTCAGGA 7260



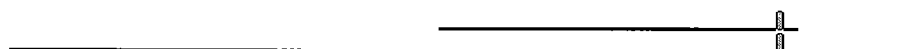
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 3272 GAGACAATGAATTAATGAGGAGCATATGGGGAAGGTGGCTGAGGGTCCCTGACTTACCTT 3331
|||||
Sbjct 7441 GAGACAATGAATTAATGAGGAGCATATGGGGAAGGTGGCTGAGGGTCCCTGACTTACCTT 7500



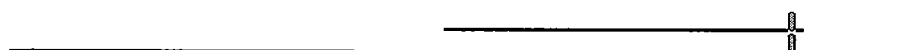
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 3332 GACCCATGGCTGAAGGCTCCATGCCCATGGCTGGAGCTGGGACCCTACACTTCTATAGTC 3391
|||||
Sbjct 7561 GACCCATGGCTGAAGGCTCCATGCCCATGGCTGGAGCTGGGACCCTACACTTCTATAGTC 7620



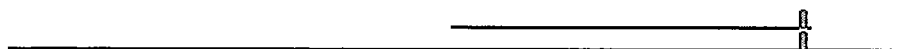
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

Query 3392 AAGGTGCTTAGCCTCAAGGTTGCAGATGCACCCTCTAGTACTCTGGGTGCAGACTGTACA 3451
|||||
Sbjct 7681 AAGGTGCTTAGCCTCAAGGTTGCAGATGCACCCTCTAGTACTCTGGGTGCAGACTGTACA 7740



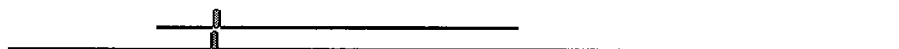
Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

```
Query 3452 CTGGGCGCAGGGGGTTGTGGAAGGACAGTGCAGATGATTCTGGGCTTTTGACACCACAGT 3511
          |||
Sbjct 7801 CTGGGCGCAGGGGGTTGTGGAAGGACAGTGCAGATGATTCTGGGCTTTTGACACCACAGT 7860
```



Score = 116 bits (60), Expect = 9e-22
Identities = 60/60 (100%), Gaps = 0/60 (0%)
Strand=Plus/Plus

```
Query 3512 TCCCCAGGGAAAGAGGCACTACTAATAAAAAACACTGACAGAAATCTCCTGGTCAAGTCT 3571
          |||
Sbjct 7921 TCCCCAGGGAAAGAGGCACTACTAATAAAAAACACTGACAGAAATCTCCTGGTCAAGTCT 7980
```



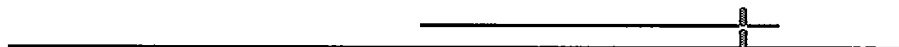
Score = 110 bits (57), Expect = 5e-20
Identities = 59/60 (98%), Gaps = 0/60 (0%)
Strand=Plus/Plus

```
Query 572 TGACATAGGGTCGGGTCGGGCAGAGCGAAGTGTAGGAGGTGATCCCCAAAGGGATGCTGG 631
          |||
Sbjct 2041 TGACATAGGGTCGGGTCGGGCAGAGCGAAGTGTAGGAAGTGTATCCCCAAAGGGATGCTGG 2100
```



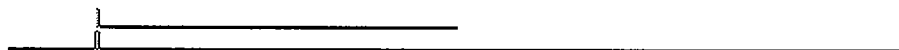
Score = 110 bits (57), Expect = 5e-20
Identities = 59/60 (98%), Gaps = 0/60 (0%)
Strand=Plus/Plus

```
Query 1712 TCCTTGAGCAGAAGACGGGGTGGGTGGGGTAGGATTGGATAGTGGTTGATGCCAAAGATT 1771
          |||
Sbjct 4321 TCCTTGAGCAGAAGACGGGGTGGGTGGGGTAGGATTGGATAGTGGTTGATGCCAAAGATT 4380
```



Score = 104 bits (54), Expect = 3e-18
Identities = 58/60 (96%), Gaps = 0/60 (0%)
Strand=Plus/Plus

```
Query 3212 TATAAGGAGAAGACTGGGCTGAGATACCTGGTGGGCTTTAGAGTAGGGGCCAGGATAA 3271
          |||
Sbjct 7321 TATAAGGAGAAAAGTGGGCTGAGATGCCCTGGTGGGCTTTAGAGTAGGGGCCAGGATAA 7380
```



Score = 62.2 bits (32), Expect = 1e-05
Identities = 32/32 (100%), Gaps = 0/32 (0%)
Strand=Plus/Plus

Query 1 ACAAACAGGAAGGACAGCAGGCTCTGGCAGCC 32
|||||
Sbjct 870 ACAAACAGGAAGGACAGCAGGCTCTGGCAGCC 901

Score = 52.6 bits (27), Expect = 0.011
Identities = 29/30 (96%), Gaps = 0/30 (0%)
Strand=Plus/Minus

Query 1585 CTCCTCCTCCTCCTCCTTCCTCCTTCTCCTC 1614
|||||
Sbjct 4172 CTCCTCCTTCTCCTCCTTCCTCCTTCTCCTC 4143

Score = 43.0 bits (22), Expect = 9.0
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

Query 1601 TCCTCCTTCTCCTCTTCCTCCT 1622
|||||
Sbjct 4171 TCCTCCTTCTCCTCTTCCTCCT 4150

CPU time: 0.24 user secs. 0.03 sys. secs 0.27 total secs.